

M. Rao



RAW SEQUENCE LISTING

DATE: 05/21/2002

PATENT APPLICATION: US/09/558,421

TIME: 14:15:59

Input Set : N:\Crif3\RULE60\09558421.raw

Output Set: N:\CRF3\05212002\I558421.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Chatterjee, Deb K.

7 (ii) TITLE OF INVENTION: Mutant DNA Polymerases and Uses Thereof

9 (iii) NUMBER OF SEQUENCES: 43

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

13 (B) STREET: 1100 New York Avenue, N.W., Suite 600

14 (C) CITY: Washington

15 (D) STATE: DC

16 (E) COUNTRY: USA

17 (F) ZIP: 20005

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25 (vi) CURRENT APPLICATION DATA:

C--> 26 (A) APPLICATION NUMBER: US/09/558,421

C--> 27 (B) FILING DATE: 26-Apr-2000

28 (C) CLASSIFICATION:

39 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/576,759

32 (B) FILING DATE:

36 (A) APPLICATION NUMBER: US 08/525,057

37 (B) FILING DATE: 08-SEP-1995

40 (A) APPLICATION NUMBER: US 08/537,397

41 (B) FILING DATE: 02-OCT-1995

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Esmond, Robert W.

45 (B) REGISTRATION NUMBER: 32,893

46 (C) REFERENCE/DOCKET NUMBER: 0942.3600002

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: 202-371-2600

50 (B) TELEFAX: 202-371-2540

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 40 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: both

59 (D) TOPOLOGY: both

61 (ii) MOLECULE TYPE: cDNA

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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68 CAGGATCCAC ATGGTGCTTA ACGGCGACAT CCACACTAAG
70 (2) INFORMATION FOR SEQ ID NO: 2:
72     (i) SEQUENCE CHARACTERISTICS:
73         (A) LENGTH: 27 base pairs
74         (B) TYPE: nucleic acid
75         (C) STRANDEDNESS: both
76         (D) TOPOLOGY: both
78     (ii) MOLECULE TYPE: cDNA
83     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
85 GTTAACTTCT TGTGCGGTCT CAATGAC
87 (2) INFORMATION FOR SEQ ID NO: 3:
89     (i) SEQUENCE CHARACTERISTICS:
90         (A) LENGTH: 11 amino acids
91         (B) TYPE: amino acid
92         (C) STRANDEDNESS: single
W--> 93         (D) TOPOLOGY: Not Relevant
95     (ii) MOLECULE TYPE: protein
100    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
102    Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly
103        1             5             10
105 (2) INFORMATION FOR SEQ ID NO: 4:
107     (i) SEQUENCE CHARACTERISTICS:
108         (A) LENGTH: 11 amino acids
109         (B) TYPE: amino acid
110         (C) STRANDEDNESS: single
W--> 111         (D) TOPOLOGY: Not Relevant
113     (ii) MOLECULE TYPE: protein
118     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
120    Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly
121        1             5             10
123 (2) INFORMATION FOR SEQ ID NO: 5:
125     (i) SEQUENCE CHARACTERISTICS:
126         (A) LENGTH: 11 amino acids
127         (B) TYPE: amino acid
128         (C) STRANDEDNESS: single
W--> 129         (D) TOPOLOGY: Not Relevant
131     (ii) MOLECULE TYPE: protein
136     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
138    Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
139        1             5             10
141 (2) INFORMATION FOR SEQ ID NO: 6:
143     (i) SEQUENCE CHARACTERISTICS:
144         (A) LENGTH: 11 amino acids
145         (B) TYPE: amino acid
146         (C) STRANDEDNESS: single
W--> 147         (D) TOPOLOGY: Not Relevant
149     (ii) MOLECULE TYPE: protein
154     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
156    Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly

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157      1          5          10
159 (2) INFORMATION FOR SEQ ID NO: 7:
161      (i) SEQUENCE CHARACTERISTICS:
162          (A) LENGTH: 4 amino acids
163          (B) TYPE: amino acid
164          (C) STRANDEDNESS: single
W--> 165          (D) TOPOLOGY: Not Relevant
167      (ii) MOLECULE TYPE: protein
172      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
174      Thr Phe Ile Tyr
175      1
177 (2) INFORMATION FOR SEQ ID NO: 8:
179      (i) SEQUENCE CHARACTERISTICS:
180          (A) LENGTH: 4 amino acids
181          (B) TYPE: amino acid
182          (C) STRANDEDNESS: single
W--> 183          (D) TOPOLOGY: Not Relevant
185      (ii) MOLECULE TYPE: protein
190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
192      Ala Ile Thr Phe
193      1
195 (2) INFORMATION FOR SEQ ID NO: 9:
197      (i) SEQUENCE CHARACTERISTICS:
198          (A) LENGTH: 4 amino acids
199          (B) TYPE: amino acid
200          (C) STRANDEDNESS: single
W--> 201          (D) TOPOLOGY: Not Relevant
203      (ii) MOLECULE TYPE: peptide
208      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
210      Thr Ile Asn Phe
211      1
213 (2) INFORMATION FOR SEQ ID NO: 10:
215      (i) SEQUENCE CHARACTERISTICS:
216          (A) LENGTH: 45 base pairs
217          (B) TYPE: nucleic acid
218          (C) STRANDEDNESS: both
219          (D) TOPOLOGY: both
221      (ii) MOLECULE TYPE: cDNA
226      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
228 TCAGGCTGCT AAAACATTCA TCTACGGTAT ACTGTATGGT TCTGG
230 (2) INFORMATION FOR SEQ ID NO: 11:
232      (i) SEQUENCE CHARACTERISTICS:
233          (A) LENGTH: 33 base pairs
234          (B) TYPE: nucleic acid
235          (C) STRANDEDNESS: both
236          (D) TOPOLOGY: both
238      (ii) MOLECULE TYPE: cDNA
243      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
245 GTAGAGGACC CCGTAATTAA TGGTCTTGCC CGC

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Input Set : N:\Crf3\RULE60\09558421.raw

Output Set: N:\CRF3\05212002\I558421.raw

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247 (2) INFORMATION FOR SEQ ID NO: 12:
249   (i) SEQUENCE CHARACTERISTICS:
250       (A) LENGTH: 11 amino acids
251       (B) TYPE: amino acid
252       (C) STRANDEDNESS: single
W--> 253       (D) TOPOLOGY: Not Relevant
255   (ii) MOLECULE TYPE: protein
260   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
262   Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly
263       1             5             10
265 (2) INFORMATION FOR SEQ ID NO: 13:
267   (i) SEQUENCE CHARACTERISTICS:
268       (A) LENGTH: 4 amino acids
269       (B) TYPE: amino acid
270       (C) STRANDEDNESS: single
W--> 271       (D) TOPOLOGY: Not Relevant
273   (ii) MOLECULE TYPE: protein
277   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
279   Met Val Asn Phe
280       1
282 (2) INFORMATION FOR SEQ ID NO: 14:
284   (i) SEQUENCE CHARACTERISTICS:
285       (A) LENGTH: 694 base pairs
286       (B) TYPE: nucleic acid
287       (C) STRANDEDNESS: double
288       (D) TOPOLOGY: both
290   (ii) MOLECULE TYPE: DNA (genomic)
293   (ix) FEATURE:
294       (A) NAME/KEY: CDS
295       (B) LOCATION: 2..694
298   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
300 G GAT CCA GAC TGG TGG ATC GTC AGT GCG GAT TAT TCC CAA ATA GAA           46
301   Asp Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu
302       1             5             10             15
304 CTC AGA ATC CTC GCT CAT CTC AGT GGT GAT GAG AAC CTT GTG AAG GCC           94
305 Leu Arg Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala
306             20             25             30
308 TTC GAG GAG GGC ATC GAT GTG CAC ACC TTG ACT GCC TCC AGG ATC TAC           142
309 Phe Glu Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr
310             35             40             45
312 AAC GTA AAG CCA GAA GAA GTG AAC GAA GAA ATG CGA CGG GTT GGA AAG           190
313 Asn Val Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys
314             50             55             60
317 ATG GTG AAC TTC TCT ATA ATA TAC GGT GTC ACA CCG TAC GGT CTT TCT           238
318 Met Val Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser
319             65             70             75
321 GTG AGA CTT GGA ATA CCG GTT AAA GAA GCA GAA AAG ATG ATT ATC AGC           286
322 Val Arg Leu Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser
323       80             85             90             95

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325 TAT TTC ACA CTG TAT CCA AAG GTG CGA AGC TAC ATC CAG CAG GTT GTT      334
326 Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val
327          100          105          110
329 GCA GAG GCA AAA GAG AAG GGC TAC GTC AGG ACT CTC TTT GGA AGA AAA      382
330 Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys
331          115          120          125
333 AGA GAT ATT CCC CAG CTC ATG GCA AGG GAC AAG AAC ACC CAG TCC GAA      430
334 Arg Asp Ile Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu
335          130          135          140
338 GGC GAA AGA ATC GCA ATA AAC ACC CCC ATT CAG GGA ACT GCG GCA GAT      478
339 Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp
340          145          150          155
342 ATA ATA AAA TTG GCT ATG ATA GAT ATA GAC GAG GAG CTG AGA AAA AGA      526
343 Ile Ile Lys Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg
344 160          165          170          175
346 AAC ATG AAA TCC AGA ATG ATC ATT CAG GTT CAT GAC GAA CTG GTC TTC      574
347 Asn Met Lys Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe
348          180          185          190
350 GAG GTT CCC GAT GAG GAA AAA GAA GAA CTA GTT GAT CTG GTG AAG AAC      622
351 Glu Val Pro Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn
352          195          200          205
354 AAA ATG ACA AAT GTG GTG AAA CTC TCT GTG CCT CTT GAG GTT GAC ATA      670
355 Lys Met Thr Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile
356          210          215          220
358 AGC ATC GGA AAA AGC TGG TCT TGA      694
359 Ser Ile Gly Lys Ser Trp Ser
360          225          230
363 (2) INFORMATION FOR SEQ ID NO: 15:
365     (i) SEQUENCE CHARACTERISTICS:
366         (A) LENGTH: 230 amino acids
367         (B) TYPE: amino acid
368         (D) TOPOLOGY: linear
370     (ii) MOLECULE TYPE: protein
372     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
374 Asp Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu
375   1          5          10          15
377 Arg Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe
378          20          25          30
380 Glu Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn
381          35          40          45
383 Val Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met
384          50          55          60
386 Val Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val
387   65          70          75          80
389 Arg Leu Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr
390          85          90          95
393 Phe Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala
394          100          105          110
396 Glu Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/558,421

DATE: 05/21/2002

TIME: 14:16:00

Input Set : N:\Crif3\RULE60\09558421.raw

Output Set: N:\CRF3\05212002\I558421.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:93 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:111 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:129 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:147 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:165 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=7
L:183 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:201 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:253 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=12
L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:460 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:478 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:499 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:526 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:562 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:580 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24
L:617 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:635 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:653 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:671 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28
L:689 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30
L:725 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=31
L:742 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32
L:760 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=33
L:778 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=34
L:805 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=35
L:823 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=36
L:841 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=37
L:862 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=38
L:880 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=39
L:898 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=40
L:916 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=41
L:934 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=42
L:951 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=43